

## pQE-30, pQE-31, and pQE-32 Vectors

Positions of elements in bases	pQE-30	pQE-31	pQE-32
Vector size (bp)	3461	3463	3462
Start of numbering at <i>Xho</i> I (CTCGAG)	1-6	1-6	1-6
T5 promoter/lac operator element	7-87	7-87	7-87
T5 transcription start	61	61	61
6xHis-tag coding sequence	127-144	127-144	127-144
Multiple cloning site	145-192	147-194	146-193
Lambda <i>t</i> <sub>0</sub> transcriptional termination region	208-302	210-304	209-303
<i>rrnB</i> T1 transcriptional termination region	1064-1162	1066-1164	1065-1163
ColE1 origin of replication	1638	1640	1639
$\beta$ -lactamase coding sequence	3256-2396	3258-2398	3257-2397

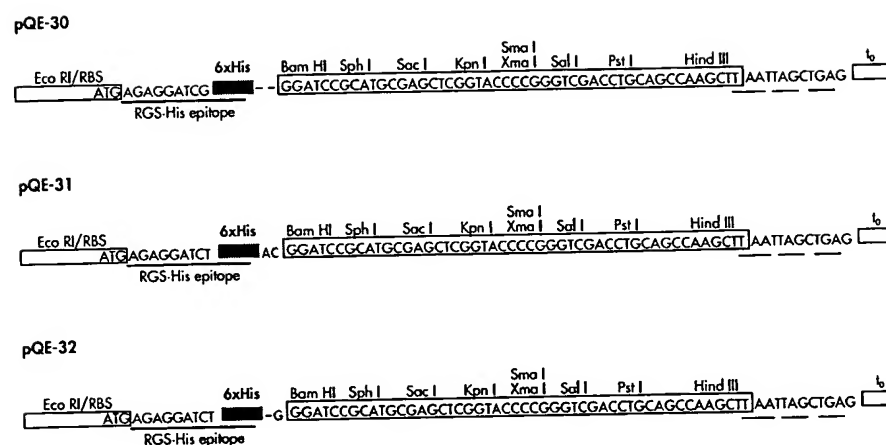
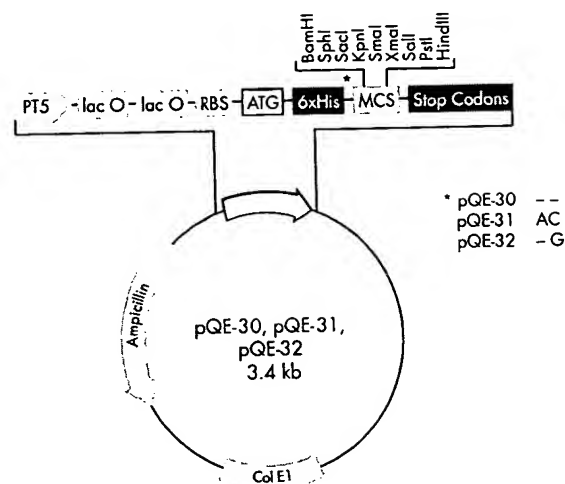


Figure 1

FIGURE 2

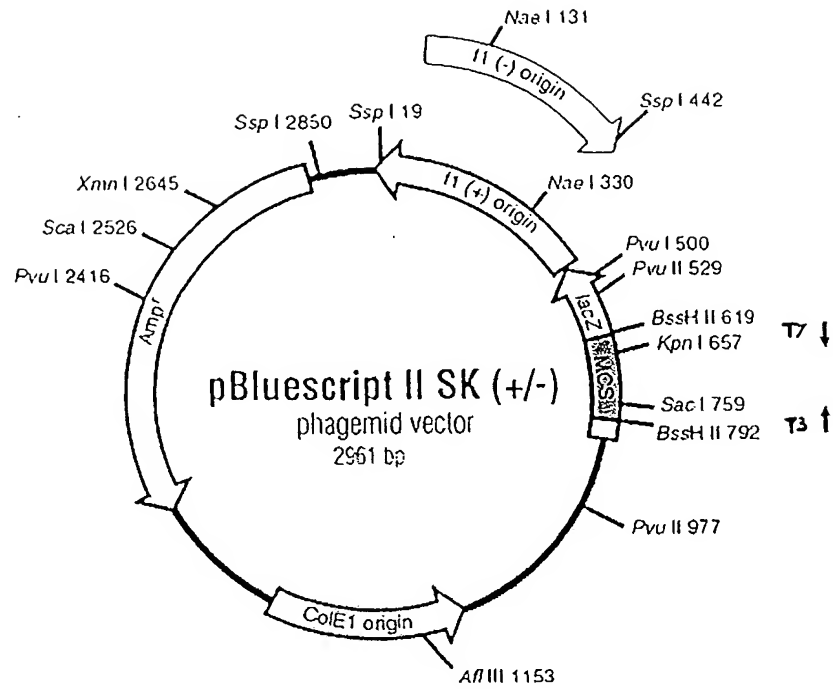
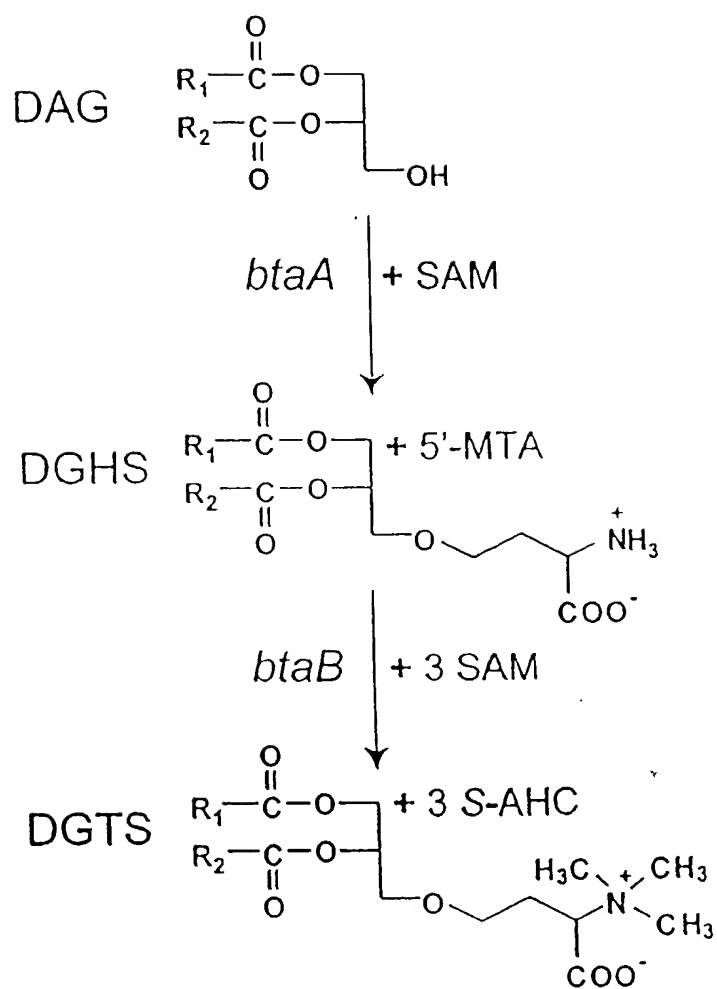


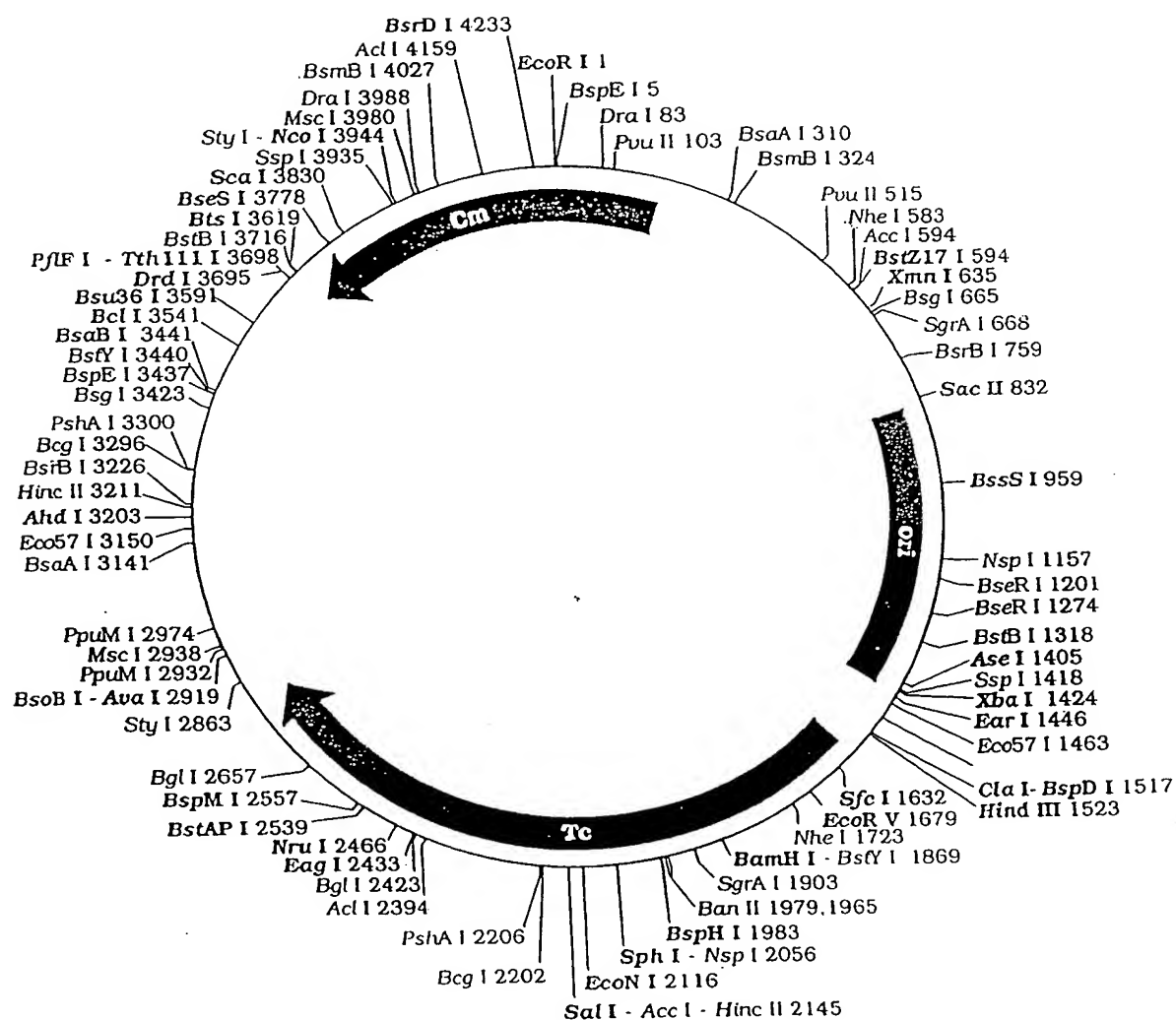
FIGURE 3



# pACYC184

4,244 base pairs  
GenBank Accession / X06403

FIGURE 4



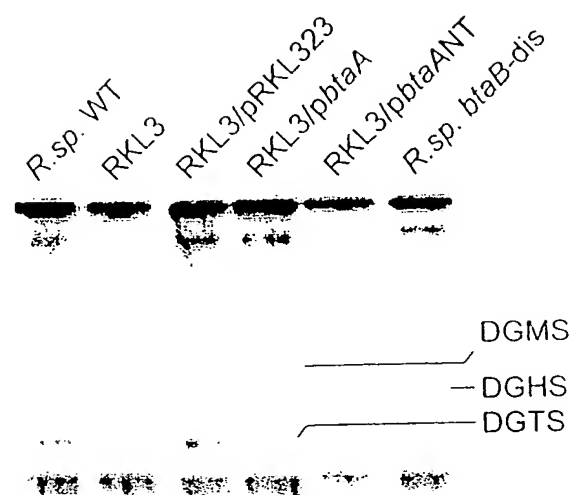


FIGURE 5

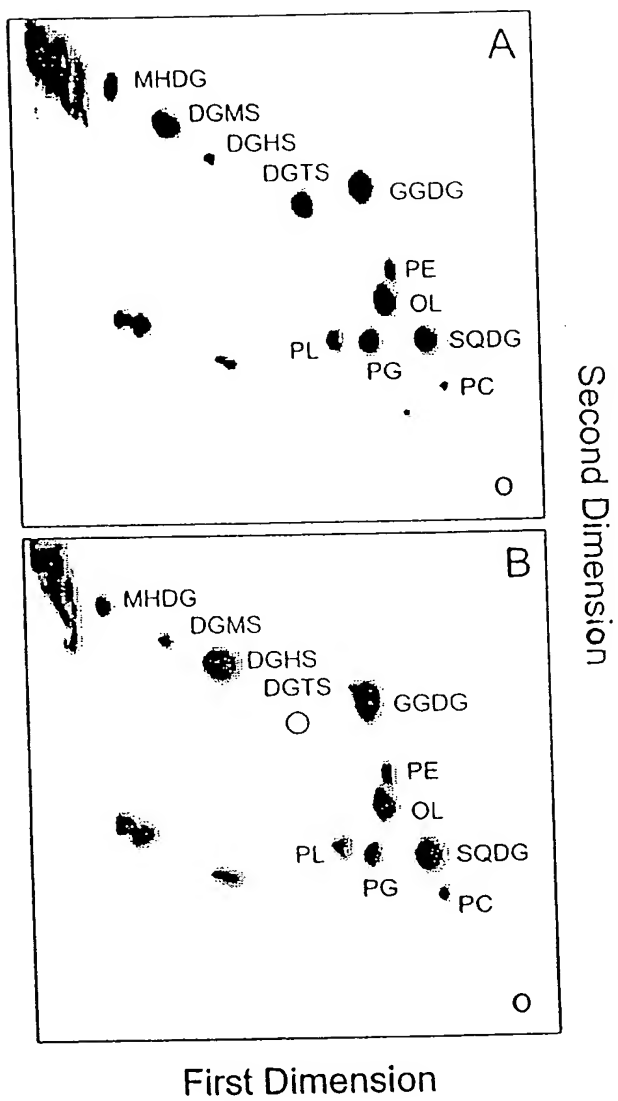


FIGURE 6

FIGURE 7

*btaA* gene cDNA Sequence

1-57           gtgacgc agttcgccct caccacactg cccgccccgc cggttgcccc ccagatcggc  
58-117       gccgccgtgc accgcacgtc gcttctcagc gccgaaggac tgatggagcg gatgttctcg  
118-177      cgcctcttcc acggcctcgt ctatccgcag atctgggagg atccggcggt ggacatggcg  
178-237      gccctcgcca tccgccccgg ggaccggctg gtggccatcg cctcgggcgg ttgcaacgtg  
238-297      ctttcctatc tcacgcaggg gccgggctcg atcctcgccg tggatctctc gcccgcccat  
298-357      gtggcgctgg ggcggtgaa gctcgccgcc gcgcggacgc tgcccgacca tgccgccttc  
358-417      ttcgaatctc tcggtcgcgc agacctgccc ggcaatgcgg ccctctacga ccgccacatc  
418-477      gcgcccgcgc tcgacggccg gagccgccgc tactgggagg cgcgcagccc cttcggccgg  
478-537      cgcatccagc tgttcgagcg cggcttctac cggcacggtg ccctcggccg cttcacggcg  
538-597      gcggcccata cgctcgcgcg ggccgcgggc accgacctgc ggggctttct cgactgtccc  
598-657      gacatcgagg cgcagcgag ctctcttac gcccatatcg ggccgctctt cgaggcgccc  
658-717      gtggtgcagg cgctcgcccg acggccggcc gcgctcttcg ggctggggat cccgcccgcg  
718-777      caatatgcgc ttctggcggg agacggcgac ggcgacgtgc tgccggtgct gcgccagcgc  
778-837      ctccaccggc tgctctgtga ctccccctg cgcgagaact acttcgcctt ccaggccatc  
838-897      gcccgccgct atccgcggcc cggcgagggc gcgctgccgc cctatctcga acccaccgcc  
898-957      ttcgagacgc tgcgcgagaa cgcgggccgg gtgcagatcg agaaccgcag cctgaccgag  
958-1017     gcgctcgcgg ccgaaccga ggagagcatc cacggcttca ccctgctcga tgcgcaggac  
1018-1077    tggatgacgg acgcgcagct gaccgcgctc tggcggcagg tgacgcgcac tgcagcgccc  
1078-1137    ggcgcgcggg tgatcttccg caccggcggg gcggccgacc tgctgcccggccgagtgcgc  
1138-1197    gaggagatcc tcgggcactg gcgcgccgac cgggcggcgg gacaggcggg ccatgccgcc  
1198-1252    gaccgttcgg cgatctacgg cggcttccac ctctaccggc ggaggggacgc catga

FIGURE 8

*btaB* gene cDNA Sequence

1-60            atgaccgacg ccacccatgc ggcgctgatg gacgcgacct accgccacca gcgccggatc  
61-120        tacgacgtca cgcggcggca ctctctgctc ggccgcgacc ggctgatcgc cgagctcgac  
121-180       ccgccccccg gcgcccgggt gctcgagatc gcctgcggca cggggcgcaa cctcgacctg  
181-240       atcgccgggc gctggcccgg ctgccggctc tcggggctcg acatctcgca ggagatgctg  
240-300       gcctcgggcc gcgcgcgtct gggccggcgc gcgacgtgg cgctcggcga tgccaccggg  
301-360       ttcgaggccc tgcccctctt cggcaccgac cggttcgagc ggatcgtcct ctctacgcg  
361-420       ctctgatga tccccgactg gcgcgaggcc ctgcgtgagg cggcgcttca tctcgtgccg  
421-480       ggggggcggc tgcattgctg cgacttcggc gatcaggcgg gcctgcccgg ctgggcccgc  
481-540       gccggcctgc gcggctggat cgggcgcttc cacgtcacgc cgcgcgacga tctgggcacg  
541-600       gcactgggcg aaacggcgct cgggatcggg ggctatgccg aataccggtc cctcggcggg  
601-660       ggatatgcga ttctcggcac gctcacgcgg tgagagatcc cctgccctgc gcgtgacgt  
661-720       tgtctccccg caggcgaccg gccgcgcgac ggccggcctg cgggcgatcc ggcgcactga  
721-780       agggccggcg cgtcgcgcgc ggggacgtag cccgcagcgg caagcggccg acagagcctg  
781-840       acagaccgtt cacggtgcgc gctccggatc ggggtgtggag ccggtgttc agaggtcagg  
841-900       cctcgaggga aagccctctg gcccgacggg caaattgtcc gggatctcta atcgggaaat  
901-960       tggtcggagc gagaggattc gaacctccga ccccctgctc ccgaagcagg tgcgtacca  
961-1020      ggctgcgcta cgctccgacc ttggcgtgcg gattataggg tcgcgcatcc gaatgcaagg  
1021-1080     gggtcggaac gcaattcgct acggagtgtc tcgcgtctcg cggcggcgca gaaggcgcgg  
1081-1140     catgaggccc acctcgggcc gcaggcgcgt ctggctcgcc gggcggttct ccgacacgtt  
1141-1200     gcggcgcgat tcgcggccga cgatalagag gccgctcgcg atgatgacct ccgccccgac  
1201-1255     ccagggtccag acgtcggacc gctcgcgaa gatgagccag ccgaagatcc ctgac

## FIGURE 9

### *btaA* gene Amino Acid Sequence

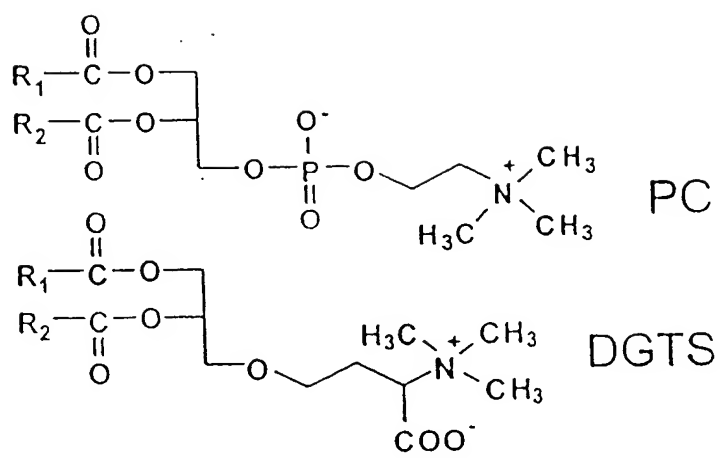
1-50 MTQFALTHLP APPVARQIGA AVHRTSLLSA EGLMERMFSS LFHGLVYPQI  
51-100 WEDPAVDMAA LAIRPGDRLV AIASGGCNVL SYLTQGPGSI LAVDLSPAVAL  
101-150 GRLKLAAART LPDHAAFFDL FGRADLPGNA ALYDRHIAPA LDGRSRRYWE  
151-200 ARSPFGRRIQ LFERGFYRHG ALGRFIGAAH TLARAAGTDL RGFLDCPDIE  
201-250 AQRSFFYAH I GPLFEAPVVQ ALARRPAALF GLGIPPAQYA LLAGDGDGDV  
251-300 LPVLRQRLHR LLCDFPLREN YFAFQAIARR YPRPGEGALP PYLEPTAFET  
301-350 LRENAGRVQI ENRSLTEALAA EPEESIHGFT LLDAQDWMTD AQLTALWRQV  
351-400 TRTAAPGARV IFRTGGAADL LPGRVPPEIL GHWRADRAAG QAGHAADRSA  
401-413 IYGGFHLYRR RDA

## FIGURE 10

### *btaB* gene Amino Acid Sequence

1-50 MTDATHAALM DATYRHQRRY YDVTRRHFL GRDRLIAELD PPPGARVLEI  
51-100 ACGTGRNLDL IGRRWPGCRL SGLDISQEML ASARARLGRR ATLALGDATR  
101-150 FEALPLFGTD RFERIVLSYA LSMIPDWREA LREAALHLVP GGRLHVVDG  
151-200 DQAGLPGWAR AGLRGWIGRF HVTPRDDLGT ALGETALGIG GYAEYRSLGG  
201-210 GYAILGTLTR

FIGURE 11



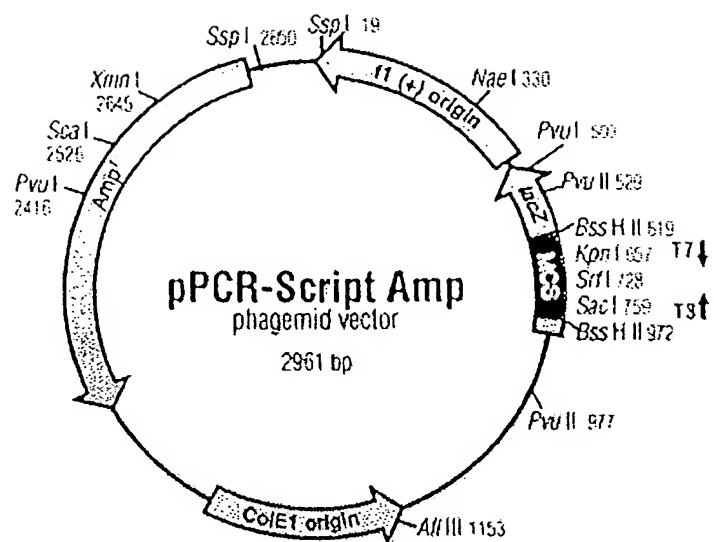
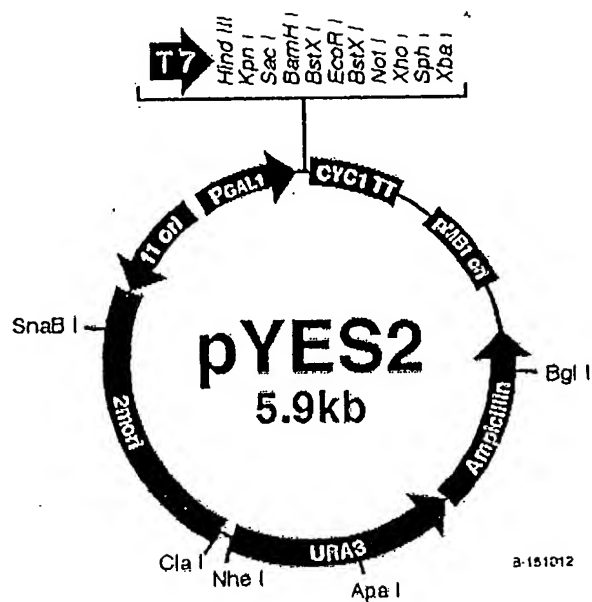


FIGURE 12

Comments for pYES2:  
 5867 nucleotides

FIGURE 13

GAL1 promoter: bases 1-452  
 T7 promoter/printing site: bases 476-495  
 Multiple cloning site: bases 502-601  
 CYC1 transcription terminator: bases 608-857  
 pMB1 (pUC-derived) origin: bases 1039-1712  
 Ampicillin resistance gene: bases 1857-2717  
 URA3 gene: bases 2735-3842  
 2 micron origin: bases 3840-5317  
 f1 origin: bases 5385-5840



## FIGURE 14

Mutagenesis Oligonucleotide btaA-L9I

5'-CGC CCT CAC CCA CAT TCC CGC CCC GC-3'

and its reverse complement:

5'-GCG GGG CGG GAA TGT GGG TGA GGG CG-3'

## FIGURE 15

Mutagenesis Oligonucleotide btaA-A201G

5'-GAC TGT CCC GAG ATC GAG GGC CAG CGC CAG C-3'

and its reverse complement:

5'-GCT GGC GCT GGC CCT CGA TCT CGG GAC AGT C-3'

## FIGURE 16

Mutagenesis Oligonucleotide btaA-S399T

5'-GCC GCC GAC CGT ACG GCG ATC TAC GG-3'

and its reverse complement:

5'-CCG TAG ATC GCC GTA CGG TCG GCG GC-3'

## FIGURE 17

Mutagenesis Oligonucleotide btaB-T13S

5'-GCT GAT GGA CGC GTC CTA CCG CCA CCA G-3'

and its reverse complement:

5'-CTG GTG GCG GTA GGA CGC GTC CAT CAG C-3'

## FIGURE 18

Mutagenesis Oligonucleotide btaB-I115L

5'-CGG TTC GAG CGG CTC GTC CTC TCC TAC GC-3'

and its reverse complement:

5'-GCG TAG GAG AGG ACG AGC CGC TCG AAC CG-3'

## FIGURE 19

Mutagenesis Oligonucleotide btaB-G206A

5'-GGA TAT GCG ATT CTC GCC ACG CTC ACG CG-3'

and its reverse complement:

5'-CGC GTG AGC GTG GCG AGA ATC GCA TAT CC-3'

RsBtaA	1	MTQFALTHLPAPPVVARQTCAAVHRTSLLSAEGEMERVESRLFHGLVYPQIWEDPAVDMAA
MlBtaA	1	MT--DVSSDLVFRRGKEVCKAVYQNRALSKAGISERIEAFLESLGLVYPQIWEDPDVDMBA
consensus	1	mt lt ar iG AV LS Gl ERmF LF GLVYPQIWEDP VDM A
RsBtaA	61	LAIRPGDRIVA IASGGCNVLSYLTQCFESILAVDLSPAHVVALGRUKLAAARTLPDHAFF
MlBtaA	59	MOIGQGHRIIVT IASGGCNILAYLTRSPTRIDAVDLNAAHTALNRVKLEAVRRLPSQGLF
consensus	61	l i G RlV IASGGCNvL YLT Pg I AVDL AHvAL RlKL A R LP a F
RsBtaA	121	DLFCRADLPGNAALYDRHIAPALDGRSRYWEARSPPG-RRIOIFERGFYRHGALGRFIC
MlBtaA	119	RFFCAADTSHNSQAYDRFIAPHLDPVSRHYWERRNWRGRRRIAVDRNFYOTGLGLFIA
consensus	121	FG AD N YDR IAP LD SRyWE R G RRI lFeR FY G LG FIg
RsBtaA	180	AATLARAACDLDLGRFLDCPDIEAQRSEFFYAHICPIFEAPVWQALARRPAALFGLGIPPA
MlBtaA	179	MCHRTAKFFCVNPAHMMIARNIGEORRFFNEEIGAPVFDKKLWKWATSRKASLFGLGIPPA
consensus	181	aH Ar G ld I QR FF igPlFe vv R A LFGLGIPPA
RsBtaA	240	QYALLAGDGDGVVLRRLRHLRLCDFPLRENYFAFOAIARRYPRPGEALPPYLEPTA
MlBtaA	239	QYDSLITSGDGTMASVLRARLEKLCDFPLENNYFAFOAFARRYPNPGEAALPAYLEKQN
consensus	241	QY L GDG v VLR RL rL CDFPL NYFAfQA ARRYP PGEgALP YLE
RsBtaA	300	FETIRENAGRVOIENRSLIEALAAPEESTHGFLLDQAQDWMTDAQLTALWROVIRTAAP
MlBtaA	299	YETIRGNIDRVAIHHANLIEFLACKDAGIVDRFILLDQAQDWMTDDQLNALWSEISRTASA
consensus	301	fETlR N RV I L E Laa si F LLDAQDWMTD QL ALW vtrTA
RsBtaA	360	GARVIFRTGGAAADLLPGRVPEEILGHWRADRAAGQAGHAADRSATYGGFHLYRRRDA
MlBtaA	359	GARVIFRTAAEPSLLPGRVSTSLDDQWDYQDEASREFSARDRSATYGGFHLYVVRTA
consensus	361	GARVIFRTgg LLPGRV iL W A A DRSAIYGGFHLY rR A

FIGURE 20

RsBtaB	1	-----MTDATHAALMDATYRHHORRIYDVTRRHELLGRDRLLAELEPPPGARVLEIAC
MlBtaB	1	MTELPASPEFKANHAELMDEVVYHWORHIYDVTRKYVLLGRDRLLDGLLEVPOGETVLELGC
consensus	1	A HA LMDa Yr QRrIYDvTRr fLLGRDRLLI Ld P Ga VLEIaC
RsBtaB	53	GTGRNLDLIGRRAPGCRLSGLDISQEMLASARARLGRR-----ATLALGDATRFESALPLF
MlBtaB	61	GTGRNIIILAARRVDPARFFGLDISAEMLETAGKADREGLSGHVTLTRGDATDFHAAALY
consensus	61	GTGRNl L gRRwP R GLDIS EML sA l R TL GDAT FeA Lf
RsBtaB	108	GTDRFERIVLSYALSMIPDWREARREAAHLVPGGRLHVVDGQOAGLPGWARAGLRGWI
MlBtaB	121	GIERFORNFVSYSLSMIPGWKEKTSAAALASPNGLHIVVDGQOQGLPGWFRTLLRGWI
consensus	121	G dRFeRi lSY LSMIP W l A L P G LHvVDG Q GLPGW R LRGWi
RsBtaB	168	GRFHVTPRDDLGTALGETALGIGCYAEMRSLGCGYAILGTLTR--
MlBtaB	181	KKFHVTPRESLREVLESESRRTCATFRERILYRCYAWLAMIKIAS
consensus	181	rFHVTPRd L L Gg yRsL GYA Lg l

FIGURE 21

Ml-*biaA* gene sequence

269421 atgacggacgtctcctcggatctggttttcgcgcggcaa  
269461 ggaagttggaaaggccgtctaccagaaccgcgcgtttccaaagccggcatctccgagcg  
269521 gctgttcgccttctgtttccggcctcgtctalccgcagatctgggaagaccccgatgt  
269581 cgacatggaggccatgcagcttggtcagggccatcgcacgtcacaatcgctccggcgg  
269641 ctgcaacatcctcgcctacctcacccgttcgcgggcacggatcgacgccgtcgacctcaa  
269701 cgccgccacatcgcgtgaaccgcgtgaagctggaggcgggtgcgccgtcgcctcgca  
269761 gggcgatctgttcgcgttttcggcgccgacaccagccacaattcgcaagcctatga  
269821 ccgctttattgcgccgatctcgatccggtcagccgccactattgggagcgccgcaactg  
269881 gcgtgtcgccggcgcatcgccgtcttcgaccgcaatttctaccagaccggcctgctcgg  
269941 cctgttcacgccatgggccatgcacggcgaaattcttcggcgtcaaccggcccacat  
270001 gatggaagccaggaatatcggcgagcagcgccgttcttcaacgaggagctggcgccggt  
270061 cttcgacaagaagcttttgaatggcgacctcgcgtaaggcctcgctgttcggcctcgg  
270121 cattccggcgcgagtagcattccctgatcacctcaggcgacggcaccatggccagcgt  
270181 tctgaaggcccggctggaaaagctcgctgcgattttcccctggaaaacaattatttcgc  
270241 ctggcaggcttttcccgcctatccaaatcccggtagggccgcctgcccgcctatct  
270301 ggaaaagcagaactacgaaaccatccgcggcaatcgcaccgctcgccatccaccatgc  
270361 caatctgatcgaattcctcgcggcaaggacgcgggcaccgtcgatcgcttcacctcgt  
270421 cgatgcgcaggactggatgaccgatgaccagctcaacgcgctgttggtcggaatcagccg  
270481 caccgctccgcaggcgcccgctcatcttcgcaccgccgagcccagcctgctgcc  
270541 aggccgcgtctcgacctcgtgctcgaccagtgggactatcaggacgaggcgtcgcgcga  
270601 attctcggcacgcgaccgttcggccatctatggcggcttcacctctatgtgaagcgcac  
270661 ggcatga

FIGURE 22

Ml-*btaB* gene sequence

270670 atgaccgagctgccggccagccccgaattcaaggccaatcatgccgaactg  
270721 atggacggcgtctaccactggcagcgccacatctatgacctgactcgaaatactatctg  
270781 ctcggccgcgaccggctgatcgaatgggcttgaggcgcaaggcggcaccgtgctggaa  
270841 ctcggctgcggcaccggccgcaacatcatcctggccggcccgctaccctgatgcccgc  
270901 ttctcggcctggatatctcggccgagatgctggagacggccggcaaggcgatcgaccgc  
270961 gaaggcctgtccggccacgtaacgctgacacgaggcgacgccaccgatttcgacggccgcg  
271021 gcactttacggcatcgagcgcttcgaccgctcttcgtctcctattcgctgtcgaatgc  
271081 ccaggctgggaaaagacgggtgtcggcggcactcgccgcactatccccaacggctcgctg  
271141 cacatcgtcgatttcggccagcaggaaggcctaccgggctgggttcgtaccttgctgcgc  
271201 ggttggctgaaaaattccacgtaacgccgcgtgaatcgctgcgcgaagtctggaatcg  
271261 gaatctcggcgaaccggcgcaaccttcggttcgcacgctttatcgcggttacgcctgg  
271321 ctggcgatgatcaagatgccagctaa

FIGURE 23

FIGURE 24

*Agrobacterium tumefaciens* BtaA DNA

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1 atg acg agt gcg gca ccc aag acc ggc ttc agc aaa aac acg aaa ctg aag tcc gca ttg
61 ctc cag cac aag gca ctc tcc aaa agc ggc ttc ggc gtc gtc ctc ttt
121 tcc ggc ctc gtc tat ccg cag atc tgg gaa gac ccc gag atc gac atg gaa gcg atg gag
181 ctt ggc gaa ggc cac cgc atc gtc acc acc ggc tcc ggc ggc tgc aac atg ctc ggc tat
241 ctc tcg cgc aac ccg gtc agc atc gat gtc cat gtc gac ccc gag cac cac atc ggc ctg
301 aac aag ctg aag ctc gct ggc ttc cgc cat ctg ggt tat gac cat cag gat ttc atc gtc cac
361 ttc ggc cgc ggc acc aag gca tac agc aac agc gtc ggt gac cgt ttc ggc atc gtc gag cat
421 ctg gat gcc acc ggc acc aag gca tac tgg cgg acc ggc ctg acc ggc cgt ttc ggc atc ggc
481 tcg gtc ttc gac agc aac atc gac ggc gtc agc aag gtc ggc att ttc gac aag acc cgc gtc
541 cac atc atg gcc cgc cag ttt gac agc aag gtc ggc ctt ggc att ttc gac aag ccg gtc gtc
601 gac gaa cag cgc cag ttt gac agc aag gtc ggc ctt ggc att ttc gac aag ccg gtc gtc
661 ggc tgg ctg acg aag cgc cag ttt gac agc aag gtc ggc ctt ggc att ttc gac aag ccg gtc
721 gac gag ctg gca agc ctt tcc agc tcc gtc ctc ccg ctc aag gag ggc cag ctg
781 gaa aag ctt gcc tgc aac ttc ccg gtc gac ggc aat tat ttc ggc att ttc gac aag ccg gtc
841 ggc cgt tat ccc gag ccg cat ggc ggt gtc gtc gac ggc aat tat ttc ggc att ttc gac aag
901 gaa aag atc cgc aac aac acc ggc gtc gtc gac ggc ctg ggc gtc gac ggc aat tat acc gag
961 ctt tcc cgc aag ccg cag ggc gtc gtc gac ggc gtc gtc gac ggc aat tat acc gag
1021 atg acg gat gtc cag ctc aag ggc gtc gtc gac ggc gtc gtc gac ggc aat tat acc gag
1081 gca cgc gtc atc ttc cgc gtc gtc gac ggc gtc gtc gac ggc gtc gtc gac ggc aat tat acc
1141 gac atc cgc aac cag tgg ggc gtc gtc gac ggc gtc gtc gac ggc gtc gtc gac ggc aat tat
1201 cgc tcg gcc att tat ggc ggc ttc cat atc gac ggc gtc gtc gac ggc gtc gtc gac ggc aat

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FIGURE 25

*Agrobacterium tumefaciens* BtaA protein

MTSAAPKTGFSKNTKLKSALLQHKALSKSGLSERFFGVLFSGLVYPQIWEDPEIDMEA  
MELGEGHRIVTIGSGGCNMLAYLSRNPASIDVVDLNPHHIALNKLKLAAFRHLPAHQD  
VVRHFGRAGTRSNSVGYDRFIAEHLDATTKAYWSKRTLSGRRRISVFDRNIYRTGLLG  
RFIGAGHIMARLHGVKLTEMAKTRTLDEQRQFFDSKVAPLFDKPVVRWLTKRKSSLFG  
LGIPPRQYDELASLSSDGTVASVLKERLEKLACNFPLSDNYFAWQAFARRYPEPHEGA  
LPAYLKPEYYEKIRNNTARVAVHHATYTELLSRKPANGVDRYILLDAQDWMTDVQLNE  
LWSQISRTAASGARVIFRTAAEKSVIEGR LSPDIRNQWVYLEERSNELNAMDRSAIYG  
GFHIYQRAMA

FIGURE 26

*Agrobacterium tumefaciens* BtaB DNA

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1  atgaaaacca tcggcgagaa tgtcggcctt gcagacagcg cgcattgcggg cttgatggac
61 cgcattgata gccaccagcg ccataatctac gatatacacc gcaaatatta tcttctgggc
121 cgtgaccgga ccatttcagg cctcgacgtg ccaaagggcg gcacgctgct ggaaatcggc
181 tgcggcaccg gccgcaacct gctgctggcc agccgccggg ttcccgacgc caaactcttc
241 ggcttcgata tatcagccga aatgctgctg accgcctccg agaattttgc cggcaaagcg
301 gagcgaccca ttctgcgtgt cggcgatgcc accgctttcc ggtcttcgga attcggccag
361 cccgatggct tcgaccgcgt catgatccct tatgcgctgt cgatgatacc ggactgggaa
421 aaagcgatcg aacaggcgct cgcggcgctg aaaccggcg gttcgctgca tatcgtcgat
481 ttcggccagc aggaacagtt gccgaagtgg ttccgcacgc ttcttcaagc ctggctcacc
541 cgctttcacg ttacgccccg cgcaaatctc cgttacgttc tcgccaatat ggccggccgt
601 ttcgacggga atctcgtctt cgaggaaatc gcgaggggat acgcatggcg ggctgtcatc
661 acgcttcagg ttgccgaagc cccgcagccg aagatccacc gcttattggc tgacgcctga

```

FIGURE 27

*Agrobacterium tumefaciens* BtaB protein

MTDATHAALMDATYRHQRRIDVTRRHFLGRDRLIAELDPPPG  
ARVLEIACGTGRNLDLIGRRWPGCRISGLDISQEMLASARARLG  
RRATLALGDATRFEALPLFGTDRFERIVLSYALSMIPDWREALR  
EAALHLVPGGRLHVVDGQAGLPGWARAGLRGWIGRFHVTPRD  
DLGTALGETALGIGGYAEYRSLGGGYAILGTLTR

*Sinorhizobium meliloti* BtaA DNA

1 atg acc gac gac ttc gcc ccg gat gcc ggc ttc ggc aag aag aat ccg aaa ctg aaa agc gca  
61 ctc ctg cag cac aaa gct ctc tcc tcc ccc gcc ggc aat tcc gaa cgc ctg ttc ggg ggc ctg agc ggc  
121 ttt tcc gga ctc gtc tac ccg cag atc ccc gcc cag tcc ggg gac cgc att gtc gac ctg atg agc ggc  
181 cag atc cgt tcc gcc gag cct cag ggc atc ggc ggc cct ggc ggc ggc ggc ggc ggc ggc ggc ggc  
241 tat ctc tcc cag aag ctg tct gcc cgc ata gac gtc gat ctc aac ccc cat cag atg acc ggc ggc  
301 ctc aac cgg gcc ctg aag ggt acg cgc cgc ttt gcc ggc cag ctg cag gcc gac aag gac gtc gtc ggc  
361 ttc ctc gcc gtc gca acc cgc aac cgc tat tgg aac ggc cag gcc tac gac gtc gtc ggc ggc ggc  
421 aag ctc gat gtc ccc gca gcc ggc tat tgc ggc gat ctc ggc ggc ggc ggc ggc ggc ggc ggc  
481 atc ggc gtc gtc ctc gca ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
541 agc cat gct gtc gtc gca ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
601 atg cgc gag gtc ctc gca ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
661 atc cgt tgg gtc gtc gca ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
721 ttc gac gaa tgg gtc gtc gca ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
781 ctg gaa aag cgc tac ccc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
841 gca cgg cgc cgc att cgc cgc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
901 tac gaa gcc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
961 ctt ctc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
1021 tgg atg acc gac gac ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc  
1081 ggc ggc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc  
1141 acc acc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc  
1201 gac cgg tcg tcg ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc

FIGURE 29

*Sinorhizobium meliloti* BtaA protein

MTDFAPDAGFGKKNPKLKSALLQHKALSPAGLSERLFGLLFSGLVYPQIWEDPIVDME  
AMQIRPGHRIVTIGSGGCNMLTYLSAEPARIDVVDLNPHHIALNRLKLSAFRHLP SHK  
DVVRFLAVEGTRTNGQAYDVFLAPKLDPATRAYWNGRDLTGRRRIGVFGRNVYRTGLL  
GRFISASHALARLHGINPEDFVKARSMREQRQFFDDKLAPL FERPVIRWITSRKSSLF  
GLGIPPQQFDELASLSREKSVAAVLRNRLEKLTCHFPLRDNYFAWQAFARRYPRPDEG  
ELPPYLQASRYEAIRDNAERVEVHHASFTELLAGKPAASVDYVLLDAQDWMTDQQLN  
DLWTEITRTADAGAVVIFRTAAEASILPGRLSTTLLDQWYYDAETSMRLGAEDRSAIY  
GGFHIYRKKA

FIGURE 30

*Sinorhizobium meliloti* BtaB DNA

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1  atgagcgccg tgcagaccgc gaatgaaagc cacgctcatc tgatggaccg catgtatcgc
61 taccagcggc acatctatga ttccactcgc aaatactatc tcttcggccg tgacacgctg
121 atccgtgaac tgaacccgcc gccaggcgca tcggtgctgg aagtcggctg cggcacgggc
181 cgcaatctcg ccgtgatcgg ggatctctac cccggtgcgc gcctcttcgg cctcgatata
241 tcggccgaaa tgctggcgac cgccaaagcc aagctccggc gccaaaatcg gccggacgca
301 gtggtgcggg tcgccgacgc gacgaatttc accgccgcct cattcgatca ggaaggcttc
361 gaccggatcg tcatttccta cgccctttcc atggttcccg aatgggaaaa ggcggtcgat
421 gccgcgattg ccgcgctcaa gccggggcggc tcgctgcata tcgccgactt cggccagcag
481 gaaggttggc cggccggcct ccgccgcttc ctccaggcct ggctcagacg cttccacgtc
541 acgccgcgcg aaacgccttt cgatgtgatg cgcaaaagag ccgagagaaa cggagcggcg
601 ctcgaggtca gatcgctgag acgaggttat gcctggcttg tcgtctatcg ccgcgcggca
661 ccgtag

```

FIGURE 31

*Sinorhizobium meliloti* BtaB protein

MSAVQTANESHAPLMDRMYRYQRYIYDFTRKYYLFGRDTLIREL  
NPPPGASVLEVCGGTGRNLAVIGDLYPGARLFGLDISAEMPLATA  
KAKLRRQNRPDVLRVADATNFTAASFDQEGFDRIVISYALSMV  
PEWEKAVDAAIAALKPGGSLHIADFGQEGWPAGFRRFLQAWLR  
RFHVTPRETLDVMRKRAERNGAALEVRSLLRGYAWLVVYRRAA  
P

Figure 32

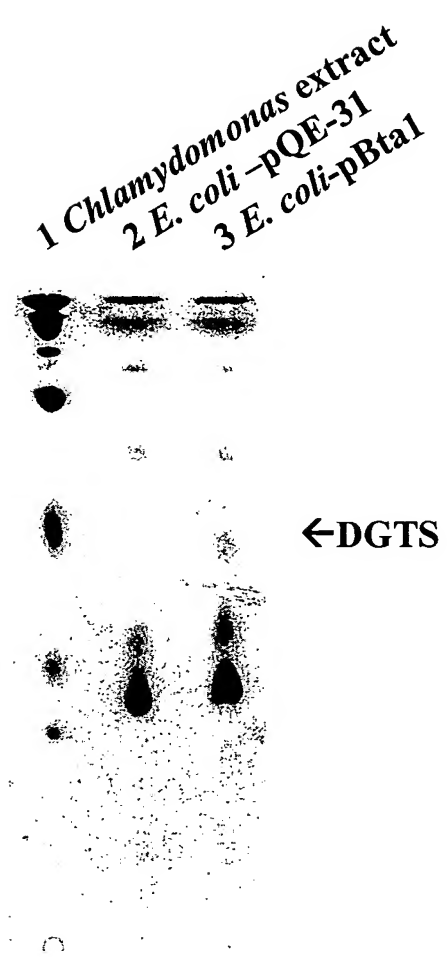


Figure 33

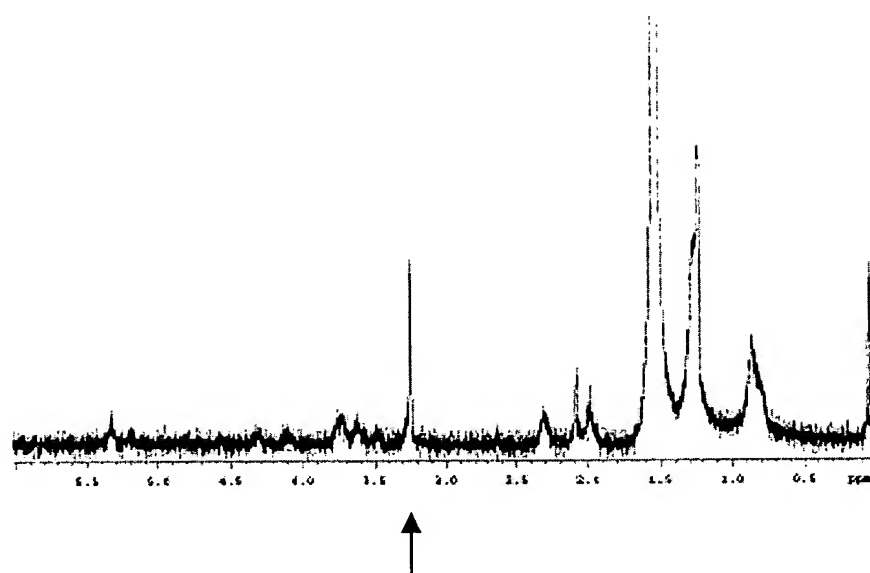
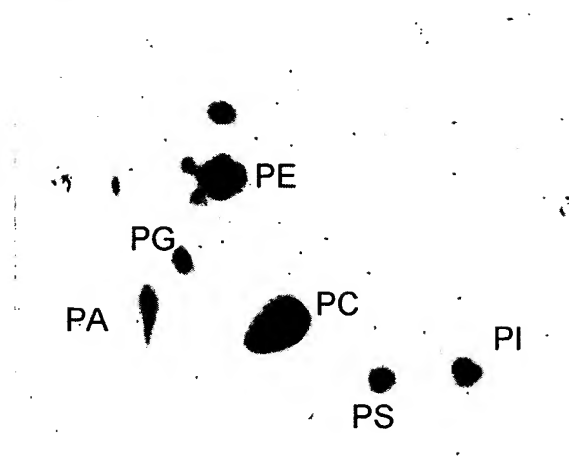


Figure 34

**A. Vogels (20 mM  $P_i$ )**



**B. Vogels -P +MES (0.01 mM  $P_i$ )**

